

## SEQUENCE LISTING

&lt;110&gt; Merck &amp; Co., Inc.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE  
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

&lt;130&gt; 21491Y PCT

&lt;150&gt; 60/548,660

&lt;151&gt; 2004-02-27

&lt;160&gt; 9

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; truncated derivative of ORF0594

&lt;400&gt; 1

Arg	Thr	Asp	Leu	Lys	Gly	Ser	Glu	Phe	Thr	Phe	Thr	Pro	Glu	Ala	Pro
1				5					10					15	
Lys	Thr	Ile	Thr	Glu	Leu	Glu	Lys	Lys	Val	Glu	Glu	Ile	Pro	Phe	Lys
		20					25					30			
Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly	Thr	Glu	Lys	Val
		35				40					45				
Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr	Thr	Pro	Thr	Leu
	50				55					60					
Lys	Asn	Pro	Leu	Thr	Gly	Val	Ile	Ile	Ser	Lys	Gly	Glu	Pro	Lys	Glu
65				70					75					80	
Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu	Thr	Glu	Tyr	Gly	Pro	Glu
			85					90					95		
Thr	Ile	Ala	Pro	Gly	His	Arg	Asp	Glu	Phe	Asp	Pro	Lys	Leu	Pro	Thr
		100					105						110		
Gly	Glu	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro	Gly	Ile	Lys	Asn	Pro	Glu
		115				120						125			
Thr	Gly	Asp	Val	Val	Arg	Pro	Pro	Val	Asp	Ser	Val	Thr	Lys	Tyr	Gly
	130				135					140					
Pro	Val	Lys	Gly	Asp	Ser	Ile	Val	Glu	Lys	Glu	Glu	Ile	Pro	Phe	Glu
145				150					155					160	
Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly	Thr	Glu	Lys	Val
			165					170					175		
Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr	Thr			
		180					185								

&lt;210&gt; 2

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; His-tagged derivative of SEQ ID NO: 1

&lt;400&gt; 2

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Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
 1          5          10          15
Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
 20          25          30
Ser Pro Asp Leu Gly Thr Asp Asp Asp Lys Ala Met Gly Arg Thr
 35          40          45
Asp Leu Lys Gly Ser Glu Phe Thr Phe Thr Pro Glu Ala Pro Lys Thr
 50          55          60
Ile Thr Glu Leu Glu Lys Lys Val Glu Glu Ile Pro Phe Lys Lys Glu
 65          70          75          80
Arg Lys Phe Asn Pro Asp Leu Ala Pro Gly Thr Glu Lys Val Thr Arg
 85          90          95
Glu Gly Gln Lys Gly Glu Lys Thr Ile Thr Thr Pro Thr Leu Lys Asn
 100         105         110
Pro Leu Thr Gly Val Ile Ile Ser Lys Gly Glu Pro Lys Glu Glu Ile
 115         120         125
Thr Lys Asp Pro Ile Asn Glu Leu Thr Glu Tyr Gly Pro Glu Thr Ile
 130         135         140
Ala Pro Gly His Arg Asp Glu Phe Asp Pro Lys Leu Pro Thr Gly Glu
 145         150         155         160
Lys Glu Glu Val Pro Gly Lys Pro Gly Ile Lys Asn Pro Glu Thr Gly
 165         170         175
Asp Val Val Arg Pro Pro Val Asp Ser Val Thr Lys Tyr Gly Pro Val
 180         185         190
Lys Gly Asp Ser Ile Val Glu Lys Glu Glu Ile Pro Phe Glu Lys Glu
 195         200         205
Arg Lys Phe Asn Pro Asp Leu Ala Pro Gly Thr Glu Lys Val Thr Arg
 210         215         220
Glu Gly Gln Lys Gly Glu Lys Thr Ile Thr Thr
 225         230         235

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&lt;210&gt; 3

&lt;211&gt; 1240

&lt;212&gt; PRT

&lt;213&gt; S. aureus

&lt;400&gt; 3

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Met Arg Asp Lys Lys Gly Pro Val Asn Lys Arg Val Asp Phe Leu Ser
 1          5          10          15
Asn Lys Leu Asn Lys Tyr Ser Ile Arg Lys Phe Thr Val Gly Thr Ala
 20          25          30
Ser Ile Leu Ile Gly Ser Leu Met Tyr Leu Gly Thr Gln Gln Glu Ala
 35          40          45
Glu Ala Ala Glu Asn Asn Ile Glu Asn Pro Thr Thr Leu Lys Asp Asn
 50          55          60
Val Gln Ser Lys Glu Val Lys Ile Glu Glu Val Thr Asn Lys Asp Thr
 65          70          75          80
Ala Pro Gln Gly Val Glu Ala Lys Ser Glu Val Thr Ser Asn Lys Asp
 85          90          95
Thr Ile Glu His Glu Pro Ser Val Lys Ala Glu Asp Ile Ser Lys Lys
 100         105         110

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Glu	Asp	Thr	Pro	Lys	Glu	Val	Ala	Asp	Val	Ala	Glu	Val	Gln	Pro	Lys	115	120	125
Ser	Ser	Val	Thr	His	Asn	Ala	Glu	Thr	Pro	Lys	Val	Arg	Lys	Ala	Arg	130	135	140
Ser	Val	Asp	Glu	Gly	Ser	Phe	Asp	Ile	Thr	Arg	Asp	Ser	Lys	Asn	Val	145	150	155
Val	Glu	Ser	Thr	Pro	Ile	Thr	Ile	Gln	Gly	Lys	Glu	His	Phe	Glu	Gly	165	170	175
Tyr	Gly	Ser	Val	Asp	Ile	Gln	Lys	Lys	Pro	Thr	Asp	Leu	Gly	Val	Ser	180	185	190
Glu	Val	Thr	Arg	Phe	Asn	Val	Gly	Asn	Glu	Ser	Asn	Gly	Leu	Ile	Gly	195	200	205
Ala	Leu	Gln	Leu	Lys	Asn	Lys	Ile	Asp	Phe	Ser	Lys	Asp	Phe	Asn	Phe	210	215	220
Lys	Val	Arg	Val	Ala	Asn	Asn	His	Gln	Ser	Asn	Thr	Thr	Gly	Ala	Asp	225	230	235
Gly	Trp	Gly	Phe	Leu	Phe	Ser	Lys	Gly	Asn	Ala	Glu	Glu	Tyr	Leu	Thr	245	250	255
Asn	Gly	Gly	Ile	Leu	Gly	Asp	Lys	Gly	Leu	Val	Asn	Ser	Gly	Gly	Phe	260	265	270
Lys	Ile	Asp	Thr	Gly	Tyr	Ile	Tyr	Thr	Ser	Ser	Met	Asp	Lys	Thr	Glu	275	280	285
Lys	Gln	Ala	Gly	Gln	Gly	Tyr	Arg	Gly	Tyr	Gly	Ala	Phe	Val	Lys	Asn	290	295	300
Asp	Ser	Ser	Gly	Asn	Ser	Gln	Met	Val	Gly	Glu	Asn	Ile	Asp	Lys	Ser	305	310	315
Lys	Thr	Asn	Phe	Leu	Asn	Tyr	Ala	Asp	Asn	Ser	Thr	Asn	Thr	Ser	Asp	325	330	335
Gly	Lys	Phe	His	Gly	Gln	Arg	Leu	Asn	Asp	Val	Ile	Leu	Thr	Tyr	Val	340	345	350
Ala	Ser	Thr	Gly	Lys	Met	Arg	Ala	Glu	Tyr	Ala	Gly	Lys	Thr	Trp	Glu	355	360	365
Thr	Ser	Ile	Thr	Asp	Leu	Gly	Leu	Ser	Lys	Asn	Gln	Ala	Tyr	Asn	Phe	370	375	380
Leu	Ile	Thr	Ser	Ser	Gln	Arg	Trp	Gly	Leu	Asn	Gln	Gly	Ile	Asn	Ala	385	390	395
Asn	Gly	Trp	Met	Arg	Thr	Asp	Leu	Lys	Gly	Ser	Glu	Phe	Thr	Phe	Thr	405	410	415
Pro	Glu	Ala	Pro	Lys	Thr	Ile	Thr	Glu	Leu	Glu	Lys	Lys	Val	Glu	Glu	420	425	430
Ile	Pro	Phe	Lys	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly	435	440	445
Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr	450	455	460
Thr	Pro	Thr	Leu	Lys	Asn	Pro	Leu	Thr	Gly	Val	Ile	Ile	Ser	Lys	Gly	465	470	475
Glu	Pro	Lys	Glu	Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu	Thr	Glu	485	490	495
Tyr	Gly	Pro	Glu	Thr	Ile	Ala	Pro	Gly	His	Arg	Asp	Glu	Phe	Asp	Pro	500	505	510
Lys	Leu	Pro	Thr	Gly	Glu	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro	Gly	Ile	515	520	525
Lys	Asn	Pro	Glu	Thr	Gly	Asp	Val	Val	Arg	Pro	Pro	Val	Asp	Ser	Val	530	535	540

Thr	Lys	Tyr	Gly	Pro	Val	Lys	Gly	Asp	Ser	Ile	Val	Glu	Lys	Glu	Glu
545					550					555					560
Ile	Pro	Phe	Glu	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly
				565					570						575
Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr
			580					585					590		
Thr	Pro	Thr	Leu	Lys	Asn	Pro	Leu	Thr	Gly	Val	Ile	Ile	Ser	Lys	Gly
		595					600					605			
Glu	Pro	Lys	Glu	Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu	Thr	Glu
	610					615					620				
Tyr	Gly	Pro	Glu	Thr	Ile	Thr	Pro	Gly	His	Arg	Asp	Glu	Phe	Asp	Pro
625					630					635					640
Lys	Leu	Pro	Thr	Gly	Glu	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro	Gly	Ile
				645					650						655
Lys	Asn	Pro	Glu	Thr	Gly	Asp	Val	Val	Arg	Pro	Pro	Val	Asp	Ser	Val
			660					665					670		
Thr	Lys	Tyr	Gly	Pro	Val	Lys	Gly	Asp	Ser	Ile	Val	Glu	Lys	Glu	Glu
		675					680						685		
Ile	Pro	Phe	Lys	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly
	690					695					700				
Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr
705					710					715					720
Thr	Pro	Thr	Leu	Lys	Asn	Pro	Leu	Thr	Gly	Glu	Ile	Ile	Ser	Lys	Gly
				725					730						735
Glu	Ser	Lys	Glu	Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu	Thr	Glu
			740					745					750		
Tyr	Gly	Pro	Glu	Thr	Ile	Thr	Pro	Gly	His	Arg	Asp	Glu	Phe	Asp	Pro
		755					760					765			
Lys	Leu	Pro	Thr	Gly	Glu	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro	Gly	Ile
	770					775					780				
Lys	Asn	Pro	Glu	Thr	Gly	Asp	Val	Val	Arg	Pro	Pro	Val	Asp	Ser	Val
785					790					795					800
Thr	Lys	Tyr	Gly	Pro	Val	Lys	Gly	Asp	Ser	Ile	Val	Glu	Lys	Glu	Glu
				805					810						815
Ile	Pro	Phe	Lys	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly
			820					825					830		
Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr
		835					840					845			
Thr	Pro	Thr	Leu	Lys	Asn	Pro	Leu	Thr	Gly	Glu	Ile	Ile	Ser	Lys	Gly
		850				855					860				
Glu	Ser	Lys	Glu	Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu	Thr	Glu
865					870					875					880
Tyr	Gly	Pro	Glu	Thr	Ile	Thr	Pro	Gly	His	Arg	Asp	Glu	Phe	Asp	Pro
				885					890						895
Lys	Leu	Pro	Thr	Gly	Glu	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro	Gly	Ile
			900					905					910		
Lys	Asn	Pro	Glu	Thr	Gly	Asp	Val	Val	Arg	Pro	Pro	Val	Asp	Ser	Val
		915					920					925			
Thr	Lys	Tyr	Gly	Pro	Val	Lys	Gly	Asp	Ser	Ile	Val	Glu	Lys	Glu	Glu
					930		935				940				
Ile	Pro	Phe	Glu	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala	Pro	Gly
945					950					955					960
Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr	Ile	Thr
				965					970						975

Thr Pro Thr Leu Lys Asn Pro Leu Thr Gly Glu Ile Ile Ser Lys Gly  
 980 985 990  
 Glu Ser Lys Glu Glu Ile Thr Lys Asp Pro Val Asn Glu Leu Thr Glu  
 995 1000 1005  
 Phe Gly Gly Glu Lys Ile Pro Gln Gly His Lys Asp Ile Phe Asp Pro  
 1010 1015 1020  
 Asn Leu Pro Thr Asp Gln Thr Glu Lys Val Pro Gly Lys Pro Gly Ile  
 1025 1030 1035 1040  
 Lys Asn Pro Asp Thr Gly Lys Val Ile Glu Glu Pro Val Asp Asp Val  
 1045 1050 1055  
 Ile Lys His Gly Pro Lys Thr Gly Thr Pro Glu Thr Lys Thr Val Glu  
 1060 1065 1070  
 Ile Pro Phe Glu Thr Lys Arg Glu Phe Asn Pro Lys Leu Gln Pro Gly  
 1075 1080 1085  
 Glu Glu Arg Val Lys Gln Glu Gly Gln Pro Gly Ser Lys Thr Ile Thr  
 1090 1095 1100  
 Thr Pro Ile Thr Val Asn Pro Leu Thr Gly Glu Lys Val Gly Glu Gly  
 1105 1110 1115 1120  
 Gln Pro Thr Glu Glu Ile Thr Lys Gln Pro Val Asp Lys Ile Val Glu  
 1125 1130 1135  
 Phe Gly Gly Glu Lys Pro Lys Asp Pro Lys Gly Pro Glu Asn Pro Glu  
 1140 1145 1150  
 Lys Pro Ser Arg Pro Thr His Pro Ser Gly Pro Val Asn Pro Asn Asn  
 1155 1160 1165  
 Pro Gly Leu Ser Lys Asp Arg Ala Lys Pro Asn Gly Pro Val His Ser  
 1170 1175 1180  
 Met Asp Lys Asn Asp Lys Val Lys Lys Ser Lys Ile Ala Lys Glu Ser  
 1185 1190 1195 1200  
 Val Ala Asn Gln Glu Lys Lys Arg Ala Glu Leu Pro Lys Thr Gly Leu  
 1205 1210 1215  
 Glu Ser Thr Gln Lys Gly Leu Ile Phe Ser Ser Ile Ile Gly Ile Ala  
 1220 1225 1230  
 Gly Leu Met Leu Leu Ala Arg Arg  
 1235 1240

&lt;210&gt; 4

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; immunogen

&lt;400&gt; 4

Met Gly Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg  
 1 5 10 15  
 Lys Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu  
 20 25 30  
 Leu Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly  
 35 40 45  
 Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr  
 50 55 60  
 Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val  
 65 70 75 80

Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu
				85					90					95	
Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val
			100					105					110		
Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln
		115					120					125			
Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His
	130					135					140				
Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp
145					150					155					160
Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg
				165					170					175	
Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser
			180					185					190		
Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu
		195					200					205			
Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile
	210					215					220				
Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser
225					230					235					240
Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu
			245						250					255	
Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu
			260					265					270		
Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr
		275					280					285			
Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro
	290					295					300				
Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys
305					310					315					320
Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val
				325					330					335	
Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val
			340					345					350		
Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val
		355					360					365			
Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val
	370					375					380				
Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly
385					390					395					400
Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr
				405					410					415	
Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val
			420					425					430		
Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg
		435					440					445			
Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn
		450				455					460				
Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala
465					470					475					480
Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys
				485					490					495	
Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys
			500					505					510		

Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr		
		515						520				525					
Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys		
		530					535					540					
Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser		
545					550					555					560		
Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala		
				565					570					575			
Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp		
			580					585					590				
Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala		
		595					600					605					
Lys	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu		
		610				615					620						
Pro	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu		
625					630					635					640		
Pro	Arg	Lys	Arg	Lys	Asn	Leu	Glu	His	His	His	His	His	His				
				645					650								

<210> 5  
 <211> 708  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleic acid encoding SEQ ID NO: 2

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 accgctgctg ctaaattcga acgccagcac atggacagcc cagatctggg taccgacgac 120  
 gacgacaagg ccatgggcag aactgacttg aaagggttcag agtttacttt tacaccagaa 180  
 gcgccaacaaa caataacaga attagaaaaa aaagttgaag agattccatt caagaaagaa 240  
 cgtaaatTTTA atccggattt agcaccaggg acagaaaaag taacaagaga aggacaaaaa 300  
 ggtgagaaga caataacgac accaactacta aaaaatccat taactggagt aattattagt 360  
 aaagggtgaac caaaagaaga gattacaaaa gatccgatta atgaattaac agaatacggg 420  
 cctgaaacaa tagcgccagg tcatcgagac gaatttgatc cgaagttacc aacaggagag 480  
 aaagaggaag ttccaggtaa accaggaatt aagaatccag aacaggaga cgtagttaga 540  
 ccgcccgtcg atagcgtaac aaaatatgga cctgtaaaag gagactcgat tgtagaaaaa 600  
 gaagagattc cattcgagaa agaacgtaaa tttaatccgg atttagcacc agggacagaa 660  
 aaagtaacaa gagaaggaca aaaagggtgag aagacaataa cgacataa 708

<210> 6  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 6  
 accggttcca tatgagagat aagaaaggac cggt 34

<210> 7  
 <211> 40  
 <212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 7

ccggcgggccc tcgagattct ttcttctacg agccaataac

40

<210> 8

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 8

gagatatacc atgggcagaa ctgacttgaa aggttcaga

39

<210> 9

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

ccggcgggccc tcgagttatg tcgttattgt cttctcacct

40